

SEQUENCE LISTING

<110> The UAB Research Foundation

MARTIN, Michael

<120> Methods and Compositions Related to
Regulation of Cytokine Production by Glycogen Synthase
Kinase 3 (GSK-3)

<130> 21085.0072P1

<140> Unassigned

<141> 2005-03-09

<150> 60/551,646

<151> 2004-03-09

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 483

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 1

```

Met Ser Gly Gly Gly Pro Ser Gly Gly Gly Pro Gly Gly Ser Gly Arg
 1           5           10           15
Ala Arg Thr Ser Ser Phe Ala Glu Pro Gly Gly Gly Gly Gly Gly Gly
          20           25           30
Gly Gly Gly Pro Gly Gly Ser Ala Ser Gly Pro Gly Gly Thr Gly Gly
      35           40           45
Gly Lys Ala Ser Val Gly Ala Met Gly Gly Gly Val Gly Ala Ser Ser
      50           55           60
Ser Gly Gly Gly Pro Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Pro
65           70           75           80
Gly Ala Gly Thr Ser Phe Pro Pro Pro Gly Val Lys Leu Gly Arg Asp
          85           90           95
Ser Gly Lys Val Thr Thr Val Val Ala Thr Leu Gly Gln Gly Pro Glu
          100          105          110
Arg Ser Gln Glu Val Ala Tyr Thr Asp Ile Lys Val Ile Gly Asn Gly
          115          120          125
Ser Phe Gly Val Val Tyr Gln Ala Arg Leu Ala Glu Thr Arg Glu Leu
          130          135          140
Val Ala Ile Lys Lys Val Leu Gln Asp Lys Arg Phe Lys Asn Arg Glu
145          150          155          160
Leu Gln Ile Met Arg Lys Leu Asp His Cys Asn Ile Val Arg Leu Arg
          165          170          175
Tyr Phe Phe Tyr Ser Ser Gly Glu Lys Lys Asp Glu Leu Tyr Leu Asn
          180          185          190
Leu Val Leu Glu Tyr Val Pro Glu Thr Val Tyr Arg Val Ala Arg His
          195          200          205
Phe Thr Lys Ala Lys Leu Thr Ile Pro Ile Leu Tyr Val Lys Val Tyr
210          215          220

```

```

Met Tyr Gln Leu Phe Arg Ser Leu Ala Tyr Ile His Ser Gln Gly Val
225          230          235          240
Cys His Arg Asp Ile Lys Pro Gln Asn Leu Leu Val Asp Pro Asp Thr
          245          250          255
Ala Val Leu Lys Leu Cys Asp Phe Gly Ser Ala Lys Gln Leu Val Arg
          260          265          270
Gly Glu Pro Asn Val Ser Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala Pro
          275          280          285
Glu Leu Ile Phe Gly Ala Thr Asp Tyr Thr Ser Ser Ile Asp Val Trp
          290          295          300
Ser Ala Gly Cys Val Leu Ala Glu Leu Leu Leu Gly Gln Pro Ile Phe
305          310          315          320
Pro Gly Asp Ser Gly Val Asp Gln Leu Val Glu Ile Ile Lys Val Leu
          325          330          335
Gly Thr Pro Thr Arg Glu Gln Ile Arg Glu Met Asn Pro Asn Tyr Thr
          340          345          350
Glu Phe Lys Phe Pro Gln Ile Lys Ala His Pro Trp Thr Lys Val Phe
          355          360          365
Lys Ser Arg Thr Pro Pro Glu Ala Ile Ala Leu Cys Ser Ser Leu Leu
          370          375          380
Glu Tyr Thr Pro Ser Ser Arg Leu Ser Pro Leu Glu Ala Cys Ala His
385          390          395          400
Ser Phe Phe Asp Glu Leu Arg Cys Leu Gly Thr Gln Leu Pro Asn Asn
          405          410          415
Arg Pro Leu Pro Pro Leu Phe Asn Phe Ser Ala Gly Glu Leu Ser Ile
          420          425          430
Gln Pro Ser Leu Asn Ala Ile Leu Ile Pro Pro His Leu Arg Ser Pro
          435          440          445
Ala Gly Thr Thr Thr Leu Thr Pro Ser Ser Gln Ala Leu Thr Glu Thr
          450          455          460
Pro Thr Ser Ser Asp Trp Gln Ser Thr Asp Ala Thr Pro Thr Leu Thr
465          470          475          480
Asn Ser Ser

```

<210> 2

<211> 420

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 2

```

Met Ser Gly Arg Pro Arg Thr Thr Ser Phe Ala Glu Ser Cys Lys Pro
1          5          10          15
Val Gln Gln Pro Ser Ala Phe Gly Ser Met Lys Val Ser Arg Asp Lys
          20          25          30
Asp Gly Ser Lys Val Thr Thr Val Val Ala Thr Pro Gly Gln Gly Pro
          35          40          45
Asp Arg Pro Gln Glu Val Ser Tyr Thr Asp Thr Lys Val Ile Gly Asn
          50          55          60
Gly Ser Phe Gly Val Val Tyr Gln Ala Lys Leu Cys Asp Ser Gly Glu
65          70          75          80
Leu Val Ala Ile Lys Lys Val Leu Gln Asp Lys Arg Phe Lys Asn Arg
          85          90          95
Glu Leu Gln Ile Met Arg Lys Leu Asp His Cys Asn Ile Val Arg Leu
          100          105          110
Arg Tyr Phe Thr Tyr Ser Ser Gly Glu Lys Lys Asp Glu Val Tyr Leu
          115          120          125

```

Asn Leu Val Leu Asp Tyr Val Pro Glu Thr Val Tyr Arg Val Ala Arg
 130 135 140
 His Tyr Ser Arg Ala Lys Gln Thr Leu Pro Val Ile Tyr Val Lys Leu
 145 150 155 160
 Tyr Met Tyr Gln Leu Phe Arg Ser Leu Ala Tyr Ile His Ser Phe Gly
 165 170 175
 Ile Cys His Arg Asp Ile Lys Pro Gln Asn Leu Leu Leu Asp Pro Asp
 180 185 190
 Thr Ala Val Leu Lys Leu Cys Asp Phe Gly Ser Ala Lys Gln Leu Val
 195 200 205
 Arg Gly Glu Pro Asn Val Ser Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala
 210 215 220
 Pro Glu Leu Ile Phe Gly Ala Thr Asp Tyr Thr Ser Ser Ile Asp Val
 225 230 235 240
 Trp Ser Ala Gly Cys Val Leu Ala Glu Leu Leu Leu Gly Gln Pro Ile
 245 250 255
 Phe Pro Gly Asp Ser Gly Val Asp Gln Leu Val Glu Ile Ile Lys Val
 260 265 270
 Leu Gly Thr Pro Thr Arg Glu Gln Ile Arg Glu Met Asn Pro Asn Tyr
 275 280 285
 Thr Glu Phe Lys Phe Pro Gln Ile Lys Ala His Pro Trp Thr Lys Val
 290 295 300
 Phe Arg Pro Arg Thr Pro Pro Glu Ala Ile Ala Leu Cys Ser Arg Leu
 305 310 315 320
 Leu Glu Tyr Thr Pro Thr Ala Arg Leu Thr Pro Leu Glu Ala Cys Ala
 325 330 335
 His Ser Phe Phe Asp Glu Leu Arg Asp Pro Asn Val Lys Leu Pro Asn
 340 345 350
 Gly Arg Asp Thr Pro Ala Leu Phe Asn Phe Thr Thr Gln Glu Leu Ser
 355 360 365
 Ser Asn Pro Pro Leu Ala Thr Ile Leu Ile Pro Pro His Ala Arg Ile
 370 375 380
 Gln Ala Ala Ala Ser Pro Pro Ala Asn Ala Thr Ala Ala Ser Asp Thr
 385 390 395 400
 Asn Ala Gly Asp Arg Gly Gln Thr Asn Asn Ala Ala Ser Ala Ser Ala
 405 410 415
 Ser Asn Ser Thr
 420

<210> 3

<211> 2189

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 3

gcggcgcggc	ctggaagagg	ccagggcccg	ggggaggcgg	cggcagcggc	ggcggctggg	60
gcagcccggg	cagcccgagc	cccgcagcct	gggcctgtgc	tcggcgccat	gagcggcggc	120
gggccttcgg	gaggcgcccc	tgggggctcg	ggcagggcgc	ggactagctc	gttcgcggag	180
cccggcggcg	gaggcgagg	aggcggcggc	ggccccggag	gctcggcctc	cggcccaggc	240
ggcaccggcg	gcggaaaggc	atctgtcggg	gccatgggtg	ggggcgctcg	ggcctcgagc	300
tccgggggtg	gacccggcgg	cagcggcgga	ggaggcagcg	gaggccccgg	cgcaggcact	360
agcttcccgc	cgcccggggt	gaagctgggc	cgtgacagcg	ggaagggtgac	cacagtcgta	420
gccactctag	gccaaggccc	agagcgctcc	caagaagtgg	cttacacgga	catcaaagtg	480
attggcaatg	gctcatttgg	ggtcgtgtac	caggcacggc	tggcagagac	cagggaaacta	540
gtcgccatca	agaaggttct	ccaggacaag	aggttcaaga	accgagagct	gcagatcatg	600
cgtaagctgg	accactgcaa	tattgtgagg	ctgagatact	ttttctactc	cagtggcgag	660
aagaaagacg	agctttacct	aaatctgggtg	ctggaatatg	tgcccagagac	agtgtaccgg	720

gtggcccgcc	acttcaccaa	ggccaagttg	accatcccta	tcctctatgt	caaggtgtac	780
atgtaccagc	tcttccgcag	cttggcctac	atccactccc	agggcgtgtg	tcaccgcgac	840
atcaagcccc	agaacctgct	ggtggaccct	gacactgctg	tcctcaagct	ctgcgatttt	900
ggcagtgcaa	agcagttggt	ccgaggggag	cccaatgtct	cctacatctg	ttctcgctac	960
taccggggccc	cagagctcat	ctttggagcc	actgattaca	cctcatccat	cgatgtttgg	1020
tcagctggct	gtgtactggc	agagctcctc	ttggggccagc	ccatcttccc	tggggacagt	1080
ggggtggacc	agctggtgga	gatcatcaag	gtgctgggaa	caccaacccg	ggaacaaatc	1140
cgagagatga	accccaacta	cacggagttc	aagttccctc	agattaaagc	tcacccctgg	1200
acaaaggtgt	tcaaactctg	aacgccgcca	gaggccatcg	cgctctgctc	tagcctgctg	1260
gagtacaccc	catcctcaag	gctctcccca	ctagaggcct	gtgcgcacag	cttctttgat	1320
gaactgcat	gtctgggaac	ccagctgcct	aacaaccgcc	cacttcccc	tctcttcaac	1380
ttcagtgtctg	gtgaactctc	catccaaccg	tctctcaacg	ccattctcat	ccctcctcac	1440
ttgaggtccc	cagcgggcca	taccacctc	acccgctcct	cacaagcttt	aactgagact	1500
ccgaccagct	cagactggca	gtcgaccgat	gccacaacta	cctcactaa	ctcctcctga	1560
gggccccacc	aagcaccctt	ccacttccat	ctgggagccc	caagaggggc	tgggaagggg	1620
ggccatagcc	catcaagctc	ctgccctggc	tggggcccta	gactagaggg	cagaggtaaa	1680
tgagtccctg	tccccacctc	cagtccctcc	ctcaccagcc	tcacccctgt	ggtgggcttt	1740
ttaagaggat	tttaactggt	tgtggggagg	gaagagaagg	acaggggtgt	ggggggatga	1800
ggacctccta	cccccttggc	cccctccct	ccccagacc	tccacctcct	ccagaccccc	1860
tccccctcctg	tgtcccttgt	aaatagaacc	agcccagccc	gtctcctctt	cccttccctg	1920
gcccccggtg	gtaaatagat	tgttataatt	tttttcttaa	agaaaacgtc	gatttcgacc	1980
gtccaacctg	gccccgcccc	tcctacagct	gtaactcccc	tcctgtcctc	tgcccccaag	2040
gtctactccc	tcttcacccc	accctggagg	gccaggggag	tggagagagc	tcctgatgtc	2100
ttagtttcca	cagtaagggt	tgcctgtgta	cagacctccg	ttcaataaat	tattggcatg	2160
aaaacctgaa	aaaaaaaaaa	aaaaaaaaaa				2189

<210> 4

<211> 1639

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 4

atcatctata	tgttaaatat	ccgtgccgat	ctgtcttgaa	ggagaaatat	atcgcttggt	60
ttgtttttta	tagtatacaa	aaggagtga	aagccaagag	gacgaagtct	ttttcttttt	120
cttctgtggg	agaacttaat	gctgcattta	tcgttaacct	aacaccccaa	cataaagaca	180
aaaggaagaa	aaggaggaag	gaaggaaaag	gtgattcgcg	aagagagtga	tcatgtcagg	240
gcggcccaga	accacctcct	ttgcggagag	tgccaagccg	gtgcagcagc	cttcagcttt	300
tggcagcatg	aaagtttagc	gagacaagga	cggcagcaag	gtgacaacag	tgggtggcaac	360
tcctgggcag	ggtccagaca	ggccacaaga	agtcagctat	acagacacta	aagtgattgg	420
aaatggatca	tttgggtgtg	tatatcaagc	caaactttgt	gattcaggag	aactggtcgc	480
catcaagaaa	gtattgcagg	acaagagatt	taagaatcga	gagctccaga	tcatgagaaa	540
gctagatcac	tgtaacatag	tccgattgcg	ttatttcttc	tactccagtg	gtgagaagaa	600
agatgaggtc	tatcttaaat	tgggtgctgga	ctatgttccg	gaaacagtat	acagagttgc	660
cagacactat	agtcgagcca	aacagacgct	ccctgtgatt	tatgtcaagt	tgtatatgta	720
tcagctgttc	cgaagtttag	cctatatcca	ttcctttgga	atctgccatc	gggatattaa	780
accgcagaac	ctcttggttg	atcctgatac	tgctgtatta	aaactctgtg	actttggaag	840
tgcaaagcag	ctgggtccgag	gagaacccaa	tgtttcgtat	atctgttctc	ggtactatag	900
ggcaccagag	ttgatctttg	gagccactga	ttatacctct	agtatagatg	tatgggtctgc	960
tggctgtgtg	ttggctgagc	tgttactagg	acaaccaata	tttccagggg	atagtgggtgt	1020
ggatcagttg	gtagaaataa	tcaaggctct	gggaactcca	acaagggagc	aaatcagaga	1080
aatgaaccca	aactacacag	aatttaaat	ccctcaaatt	aaggcacatc	cttggactaa	1140
ggattcgtca	ggaacaggac	atttcacctc	aggagtgcgg	gtcttccgac	cccgaactcc	1200
accggaggca	attgcaactgt	gtagccgtct	gctggagtat	acaccaactg	cccgactaac	1260
accattggaa	gcttgtgcac	attcattttt	tgatgaatta	cgggacccaa	atgtcaaact	1320
accaaatggg	cgagacacac	ctgcactctt	caacttcacc	actcaagaac	tgtcaagtaa	1380
tccacctctg	gctaccatcc	ttattcctcc	tcattgctcg	attcaagcag	ctgcttcaac	1440
ccccacaaat	gccacagcag	cgtcagatgc	taatactgga	gaccgtggac	agaccaataa	1500

tgctgcttct	gcatcagctt	ccaactccac	ctgaacagtc	cogagcagcc	agctgcacag	1560
gaaaaaccac	cagttacttg	agtgtcactc	agcaacactg	gtcacgtttg	gaaagaatat	1620
taaaaaaaaa	aaaaaaaaa					1639

<210> 5

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 5

gggggacgat cgtcggggggg 20

<210> 6

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 6

gggggagcat gctgcggggg 20